

Result	Query
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100	100

1 GAATTCGGGACCGCCGACGAGCAGCTGTCGAGCCATGCTGAAGGGGAAATGACCA 60

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	601.8	94.3	1172	13	BX44567	BX44567 BX44567
2	569.8	90.4	832	12	B1869731	B1869731 6013936521
3	575.9	89.2	1057	11	BQ067949	BQ067949 AGENCOUNC
4	567	88.9	1014	12	BM080905	BM080905 AGENCOUNC
5	560.8	87.9	878	12	B1753845	B1753845 6030275545
6	559.8	87.7	821	12	B1598390	B1598390 6032500959
7	511.4	80.2	534	9	A1590707	A1590707 CMSCOL.X
8	501.6	78.6	714	12	BQ706612	BQ706612 6026667412
9	437.6	68.6	472	9	A1075659	A1075659 oy2c0d2.8
10	434.6	68.1	3404	11	AK035510	AK035510 Mus musc
11	425.4	66.7	843	12	B1692283	B1692283 6013427585
12	424.2	66.5	461	10	B956685	B956685 RCL-MN002
13	420.6	65.9	2206	11	BC027001	BC027001 Mus musc
14	408.2	64.0	663	9	A1193281	A1193291 uc95c07.y
15	404	63.0	855	12	B1331990	B1331990 602984339
16	402.2	63.0	750	13	B0627743	B0627743 UI-H-FC04
17	401.2	62.9	508	29	CG5633840	CG5633840 OST1333984
18	385.4	60.4	536	29	CG565930	CG565930 OST13333984
19	385.2	60.4	631	10	BB827624	BB827624 BB827624
20	385.2	60.4	689	9	A1663400	A1663400 uk12d07.y
21	356	55.8	813	10	BF532970	BF532970 602073149
22	354.6	55.6	611	11	B9040197	B9040197 AGENCOUNC
23	328.6	51.5	366	10	B9568624	B9568624 CM1-MN02
24	327.4	51.3	503	10	BP443355	BP443355 229028 M
25	323.6	50.7	485	29	CG5454707	CG5454707 OST1685939
26	320.6	50.3	522	14	CD0701495	CD0701495 EST18019
27	316.8	49.7	529	29	CG529018	CG529018 OST340659
28	316.6	49.6	543	9	AA261882	AA261882 m287c09.x
29	307.8	48.2	395	14	CB773841	CB773841 AMGNMNC.C
30	302	47.3	701	12	BM795210	BM795210 UI-H-ED00
31	298.8	46.8	469	10	AM455919	AM455919 um89f609.y
32	299.2	45.8	570	12	BM466189	BM466189 BS30000909
33	291.4	45.7	570	12	B1598982	B1598982 6033479838
34	281	44.0	458	9	AA594784	AA594784 n190001.8
35	280.6	44.0	420	13	BK488304	BK488304 DXP02686C
36	279	43.7	415	9	A1008393	A1008393 g2f6c07.x
37	274.2	43.0	458	14	RS43255	RS43255 Y974f606.x
38	274	42.9	460	9	AA15793	AA15793 x630a12.z
39	273.6	42.9	424	14	H23109	H23109 yms1f12.z
40	267.4	41.9	384	9	AA338628	AA338628 cm92h02.x
41	267.8	41.2	642	10	BB629001	BB629001 BB629001
42	265.8	41.0	429	10	AA551286	AA551286 UI-R-C4-E
43	251.8	39.5	403	29	CG613113	CG613113 OST1999161
44	247	38.7	436	10	BB450804	BB450804 BB450804
45	246	38.6	309	29	CG496943	CG496943 OST17278

42 JV

RESULT	1
LOCUS	BX444567
DEFINITION	BX444567 Homo sapiens ADULT BRAIN Hom sapiens cDNA clone
CROSSING	CSOJN003P16 5-PRIME-MIDRAW sequence.
VERSION	BX444567
KEYWORDS	BX444567.1 GI.10780253 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
(bases 1 to 1173)	
REFERENCE	EST 15 MAY 2003 linear 1173 bp mRNA

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

1 (Pages 1 to 1173)
Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope

FEATURES

Bouice

Genoscope Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3201.r for
more information about this cluster, see
<http://www.genoscope.cns.fr/seq-clusters/3201.r>. Contact :
Feng Liang Email : liang@life.technet.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Paradise Avenue Genoscope sequence ID : CS0DN003DH08Q01.
Location/Qualifiers
1. 1173
/organism="Homo sapiens"
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/library="ADULT BRAIN"
/dev_stage="adult"
/clone_1lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. 5' end
cloned, double-strand cDNA was digested with Not I and
cloned into the Not I and BclRV sites of the pCMVSPORT 6
vector. library was not normalized."

ORIGIN

Query Match	94.3%	Score 601.8;	DB 13;	Length 1173;
Best Local Similarity	98.6%;	Pred. No. 6.9e-166;		
Matches 628; Conservative	0;	Mismatches 7;	Indels 2;	Gaps 2

REFERENCE
AUTHORS
TITLES
JOURNAL
1 (bases 1 to 1173)
Li, W.B., Gruber, C., Jesssee, J. and Polajec, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

RESULT 2

LOCUS	BI869731	832 bp	mRNA	linear	EST 11-OCT-2001
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